IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with <u>underlining</u> and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please AMEND claims 1-3, 25, 26, 28 and 29; and ADD claims 31-34 in accordance with the following:

1. (currently amended) A method for <u>supporting a user in</u> predicting <u>a</u> gene expression ~~sites~~ <u>site, the gene expression site being one of a cell, a tissue and an organ, said method</u> comprising:

calculating a distance between <u>a</u> first <u>gene</u> and <u>each of a plurality of</u> second genes on a genome sequence, ~~wherein~~ <u>where</u> the first gene is <u>an</u> <u>unknown gene having an unknown gene</u> expression site ~~is unknown, and~~ <u>while</u> the second ~~gene is one of a plurality of~~ <u>genes are</u> known genes ~~whose~~ <u>having known gene</u> expression sites ~~are known; and~~

determining ~~the~~ <u>a</u> first gene expression ~~sites of the first gene~~ <u>site,</u> based on the distance<u>, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation having been determined based on a sensitivity and a specificity; and</u>

<u>outputting the first gene expression site determined by said determining.</u>

2. (currently amended) The method according to claim 1, wherein ~~the calculating includes calculating~~ the distance ~~for each of the plurality of genes, and the determining includes determining the expression sites of the first gene as an expression site of at least one gene that has~~ <u>is smaller than</u> a predetermined ~~distance relation among the plurality of genes~~ <u>threshold</u>.

3. (currently amended) The method according to claim 1, wherein ~~the~~ <u>said</u> calculating includes calculating a <u>first</u> distance between ~~the~~ <u>a</u> start <u>position of a target gene and a</u> start position of the first gene<u>,</u> and <u>a second distance between</u> the start position of <u>the target gene and a start position of</u> the second gene on the genome sequence.

4. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the end position of the second gene on the genome sequence.

5. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and the end position of the second gene on the genome sequence.

6. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the start position of the second gene on the genome sequence.

7. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between first and second positions, the first position being between the start and end positions of the first gene on the genome sequence, and the second position being between the start and end positions of the second gene on the genome sequence.

8. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the start position of the second gene on the genome sequence.

9. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the end position of the second gene on the genome sequence.

10. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

11. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

Claims 12-24 (cancelled)

25. (currently amended) A computer-readable medium encoded with a computer program, ~~product~~ including computer executable instructions, for supporting a user in predicting a gene expression ~~sites~~ site, ~~wherein~~ the gene expression site being one of a cell, a tissue and an organ, and the computer executable instructions, when executed by the computer, cause the computer to perform a method comprising:

calculating a distance between a first gene and each of a plurality of second genes on a genome sequence, ~~wherein~~ where the first gene is an unknown gene having an unknown gene expression site ~~of the first gene is unknown, and~~ while the second ~~gene is one of a plurality of~~ genes ~~whose~~ are known genes having known gene expressions sites ~~are known; and~~

determining ~~the~~ a first gene expression ~~sites~~ site of the first gene, based on the distance, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation having been determined based on a sensitivity and a specificity; and

outputting the first gene expression site as determined by said determining.

26. (currently amended) The computer program product according to claim 25, wherein the ~~determining include determining the expression sites of the first gene as an expression site of at least one gene that has~~ distance is smaller than a predetermined ~~distance relation among the plurality of genes~~ threshold.

27. (cancelled)

28. (currently amended) An apparatus for supporting a user in predicting a gene expression site, where the gene expression site is one of a cell, a tissue and an organ, said apparatus comprising:

a calculation unit that calculates a distance between a first gene and each of a plurality of second genes on a genome sequence, ~~wherein~~ where the first gene is an unknown gene having an unknown gene expression site ~~of the first gene is unknown, and~~ while the second ~~gene is one of a plurality of~~ genes ~~whose~~ are known genes having known gene expression sites ~~are known~~; and

a determination unit that determines ~~the~~ a first gene expression ~~sites~~ site of the first gene, based on the distance, as a selected gene expression site of at least one of the second

genes that has a predetermined distance relation with the first gene, the predetermined distance relation having been determined based on a sensitivity and a specificity; and

an output unit that outputs the first gene expression site determined by said determination unit.

29. (currently amended) The apparatus according to claim 28, wherein ~~the calculation unit calculates~~ the distance ~~for each of the plurality of genes, and the determination unit determines the expression sites of the first gene as an expression site of at least one gene that has~~ is smaller than a predetermined ~~distance relation among the plurality of genes~~ threshold.

30. (cancelled)

31. (new) The method according to claim 1, wherein when the first site and the second site are identical, the second site is deleted from the list before being output.

32. (new) The method according to claim 1,
wherein the sensitivity is a ratio of predicted expression sites for an unknown gene to previously determined expression sites for the unknown gene determined by another method, and
wherein the specificity is a ratio of unpredicted expression sites for the unknown gene to non-expression sites for the unknown gene previously determined by the other method.

33. (new) A method of supporting a user in determining a gene expression site, comprising:
calculating a distance of an unknown gene having an unknown gene expression site from each of a plurality of known gene expression sites for known genes on a genome sequence; and
outputting a predicted gene expression site of the unknown gene based on a sensitivity, a specificity and the distance calculated between the unknown gene and at least one of the known genes.